



SEQUENCE LISTING

<110> WUCHERPFENNIG, Kai W  
STROMINGER, Jack L

<120> MONOVALENT, MULTIVALENT AND MULTIMERIC MHC BINDING  
DOMAIN FUSION PROTEINS AND CONJUGATES, AND USES  
THEREFOR

<130> HAR-005

<140> 09/248,964

<141> 1999-02-12

<150> PCT/US97/14503

<151> 1997-08-15

<150> 60/075,351

<151> 1998-02-19

<150> 60/024,077

<151> 1996-08-15

<160> 14

<170> PatentIn Ver. 2.0

<210> 1

<211> 750

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-Fos fusion

<220>

<221> CDS

<222> (1)..(735)

<220>

<221> misc\_feature

<222> (1)..(21)

<223> 3' end of secretory signal

<220>

<221> misc\_structure

<222> (22)..(594)

<223> DRA\*0101 extracellular domain

<220>

<221> misc\_feature

<222> (595)..(615)

<223> Linker sequence

<220>

<221> misc\_feature

<222> (616)..(735)

<223> Fos leucine zipper domain

<400> 1

gta tct ctc gag aaa aga gag atc aaa gaa gaa cat gtg atc atc cag 48

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TECH CENTER 1600/2900

Val Ser Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln  
 1 5 10 15

gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac 96  
 Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp  
 20 25 30

ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg  
 144  
 Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr  
 35 40 45

gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa  
 192  
 Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln  
 50 55 60

ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg  
 240  
 Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met  
 65 70 75 80

aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta  
 288  
 Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val  
 85 90 95

act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc  
 336  
 Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu  
 100 105 110

atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg  
 384  
 Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp  
 115 120 125

ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc  
 432  
 Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe  
 130 135 140

ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc  
 480  
 Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe  
 145 150 155 160

ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc  
 528  
 Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly  
 165 170 175

ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct  
 576  
 Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro  
 180 185 190

ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat  
 624

Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp  
195 200 205

aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg  
672

Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu  
210 215 220

cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc  
720

Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe  
225 230 235 240

atc ctg gcc gcc cat tgagaattct atgac  
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Ile Leu Ala Ala His  
245

<210> 2

<211> 245

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-Fos fusion

<220>

<221> misc\_feature

<222> (1)..(7)

<223> 3' end of secretory signal

<220>

<221> misc\_structure

<222> (8)..(198)

<223> DRA\*0101 extracellular domain

<220>

<221> misc\_feature

<222> (199)..(205)

<223> Linker sequence

<220>

<221> misc\_feature

<222> (206)..(245)

<223> Fos leucine zipper domain

<400> 2

Val Ser Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln  
1 5 10 15

Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp  
20 25 30

Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr  
35 40 45

Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln  
50 55 60

Gly	Ala	Leu	Ala	Asn	Ile	Ala	Val	Asp	Lys	Ala	Asn	Leu	Glu	Ile	Met	65	70	75	80
Thr	Lys	Arg	Ser	Asn	Tyr	Thr	Pro	Ile	Thr	Asn	Val	Pro	Pro	Glu	Val	85	90	95	
Thr	Val	Leu	Thr	Asn	Ser	Pro	Val	Glu	Leu	Arg	Glu	Pro	Asn	Val	Leu	100	105	110	
Ile	Cys	Phe	Ile	Asp	Lys	Phe	Thr	Pro	Pro	Val	Val	Asn	Val	Thr	Trp	115	120	125	
Leu	Arg	Asn	Gly	Lys	Pro	Val	Thr	Thr	Gly	Val	Ser	Glu	Thr	Val	Phe	130	135	140	
Leu	Pro	Arg	Glu	Asp	His	Leu	Phe	Arg	Lys	Phe	His	Tyr	Leu	Pro	Phe	145	150	155	160
Leu	Pro	Ser	Thr	Glu	Asp	Val	Tyr	Asp	Cys	Arg	Val	Glu	His	Trp	Gly	165	170	175	
Leu	Asp	Glu	Pro	Leu	Leu	Lys	His	Trp	Glu	Phe	Asp	Ala	Pro	Ser	Pro	180	185	190	
Leu	Pro	Glu	Thr	Thr	Glu	Val	Asp	Gly	Gly	Gly	Gly	Gly	Leu	Thr	Asp	195	200	205	
Thr	Leu	Gln	Ala	Glu	Thr	Asp	Gln	Leu	Glu	Asp	Glu	Lys	Ser	Ala	Leu	210	215	220	
Gln	Thr	Glu	Ile	Ala	Asn	Leu	Leu	Lys	Glu	Lys	Glu	Lys	Leu	Glu	Phe	225	230	235	240
Ile	Leu	Ala	Ala	His												245			

<210> 3

<211> 771

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-Jun fusion

<220>

<221> CDS

<222> (1)..(756)

<220>

<221> misc\_feature

<222> (1)..(21)

<223> 3' end of secretory signal

<220>

<221> misc\_feature

<222> (22)..(615)

<223> DRB1\*1501 extracellular domain

<220>

<221> misc\_feature  
 <222> (616)..(636)  
 <223> Linker sequence

<220>  
 <221> misc\_feature  
 <222> (637)..(756)  
 <223> Jun leucine zipper domain

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 Val Ser Leu Glu Lys Arg Glu Gly Asp Thr Arg Pro Arg Phe Leu Trp  
 1 5 10 15  
 cag cct aag agg gag tgt cat ttc ttc aat ggg acg gag cgg gtg cgg 96  
 Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg  
 20 25 30  
 ttc ctg gac aga tac ttc tat aac cag gag gag tcc gtg cgc ttc gac  
 144  
 Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp  
 35 40 45  
 agc gac gtg ggg gag ttc cgg gcg gtg acg gag ctg ggg cgg cct gac  
 192  
 Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp  
 50 55 60  
 gct gag tac tgg aac agc cag aag gac atc ctg gag cag gcg cgg gcc  
 240  
 Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala  
 65 70 75 80  
 gcg gtg gac acc tac tgc aga cac aac tac ggg gtt gtg gag agc ttc  
 288  
 Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe  
 85 90 95  
 aca gtg cag cgg cga gtc caa cct aag gtg act gta tat cct tca aag  
 336  
 Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys  
 100 105 110  
 acc cag ccc ctg cag cac cac aac ctc ctg gtc tgc tct gtg agt ggt  
 384  
 Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly  
 115 120 125  
 ttc tat cca ggc agc att gaa gtc agg tgg ttc ctg aac ggc cag gaa  
 432  
 Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu  
 130 135 140  
 gag aag gct ggg atg gtg tcc aca ggc ctg atc cag aat gga gac tgg  
 480  
 Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp  
 145 150 155 160

acc ttc cag acc ctg gtg atg ctg gaa aca gtt cct cga agt gga gag  
 528  
 Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu  
 165 170 175

gtt tac acc tgc caa gtg gag cac cca agc gtg aca agc cct ctc aca  
 576  
 Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr  
 180 185 190

gtg gaa tgg aga gca cgg tct gaa tct gca cag agc aag gtc gac gga  
 624  
 Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly  
 195 200 205

ggt ggc ggc ggt cgc atc gcc cgg ctc gag gaa aaa gtg aaa acc ttg  
 672  
 Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu  
 210 215 220

aaa gct cag aac tcg gag ctc gcg tcc acg gcc aac atg ctc agg gaa  
 720  
 Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu  
 225 230 235 240

cag gtg gca cag ctt aaa cag aaa gtc atg aac cat tgagaattct atgac  
 771  
 Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His  
 245 250

<210> 4  
 <211> 252  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: DR2-Jun fusion

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 <222> (1)..(7)  
 <223> 3' end of secretory signal

<220>  
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 <222> (8)..(205)  
 <223> DRB1\*1501 extracellular domain

<220>  
 <221> misc\_feature  
 <222> (206)..(212)  
 <223> Linker sequence

<220>  
 <221> misc\_feature  
 <222> (213)..(252)  
 <223> Jun leucine zipper domain

<400> 4

Val Ser Leu Glu Lys Arg Glu Gly Asp Thr Arg Pro Arg Phe Leu Trp  
1 5 10 15

Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg  
20 25 30

Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp  
35 40 45

Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp  
50 55 60

Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala  
65 70 75 80

Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe  
85 90 95

Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys  
100 105 110

Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly  
115 120 125

Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu  
130 135 140

Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp  
145 150 155 160

Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu  
165 170 175

Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr  
180 185 190

Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly  
195 200 205

Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu  
210 215 220

Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu  
225 230 235 240

Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His  
245 250

<210> 5

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR  
primer

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<210> 6  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 6  
gtcatagaat tctcaatggg cggccaggat gaactccag 39

<210> 7  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 7  
gtatctctcg agaaaagaga gggggacacc cgaccacgtt tc 42

<210> 8  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic PCR  
primer

<400> 8  
gtcatagaat tctcaatggg tcatgacttt ctgtttaag 39

<210> 9  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic,  
biotin ligase recognition sequence

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Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp  
1 5 10

<210> 10  
<211> 16



<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic,  
linker sequence

<400> 10  
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1 5 10 15

<210> 11  
<211> 1446  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: DR2-IgG fusion

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<220>  
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<223> 3' end of secretory signal

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<222> (16)..(588)  
<223> DRA\*0101 extracellular domain

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<221> misc\_feature  
<222> (589)..(609)  
<223> Linker

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<221> misc\_feature  
<222> (610)..(729)  
<223> Fos leucine zipper domain

<220>  
<221> misc\_feature  
<222> (730)..(1437)  
<223> IgG domain

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ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac ttt gat 96  
Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp  
20 25 30

ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg gtc tgg  
 144  
 Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp  
 35 40 45

cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa ggt gca  
 192  
 Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala  
 50 55 60

ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg aca aag  
 240  
 Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys  
 65 70 75 80

cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta act gtg  
 288  
 Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val  
 85 90 95

ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc atc tgt  
 336  
 Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys  
 100 105 110

ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg ctt cga  
 384  
 Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg  
 115 120 125

aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc ctg ccc  
 432  
 Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro  
 130 135 140

agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc ctg ccc  
 480  
 Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro  
 145 150 155 160

tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc ttg gat  
 528  
 Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp  
 165 170 175

gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct ctc cca  
 576  
 Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro  
 180 185 190

gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat aca ctc  
 624  
 Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp Thr Leu  
 195 200 205

caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg cag acc  
 672  
 Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln Thr

210	215	220
gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc atc ctg		
720		
Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu		
225	230	235 240
gcc gcc cat gca gca tct gag ccc aga ggg ccc aca atc aag ccc tgt		
768		
Ala Ala His Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys		
	245	250 255
cct cca tgc aaa tgc cca gca cct aac ctc ttg ggt gga cca tcc gtc		
816		
Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val		
	260	265 270
ttc atc ttc cct cca aag atc aag gat gta ctc atg atc tcc ctg agc		
864		
Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser		
	275	280 285
ccc ata gtc aca tgt gtg gtg gtg gat gtg agc gag gat gac cca gat		
912		
Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp		
	290	295 300
gtc cag atc agc tgg ttt gtg aac aac gtg gaa gta cac aca gct cag		
960		
Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln		
305	310	315 320
aca caa acc cat aga gag gat tac aac agt act ctc cgg gtg gtc agt		
1008		
Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser		
	325	330 335
gcc ctc ccc atc cag cac cag gac tgg atg agt ggc aag gag ttc aaa		
1056		
Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys		
	340	345 350
tgc aag gtc aac aac aaa gac ctc cca gcg ccc atc gag aga acc atc		
1104		
Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile		
	355	360 365
tca aaa ccc aaa ggg tca gta aga gct cca cag gta tat gtc ttg cct		
1152		
Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro		
	370	375 380
cca cca gaa gaa gag atg act aag aaa cag gtc act ctg acc tgc atg		
1200		
Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met		
	385	390 395 400

gtc aca gac ttc atg cct gaa gac att tac gtg gag tgg acc aac aac  
1248

Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn  
405 410 415

ggg aaa aca gag cta aac tac aag aac act gaa cca gtc ctg gac tct  
1296

Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser  
420 425 430

gat ggt tct tac ttc atg tac agc aag ctg aga gtg gaa aag aag aac  
1344

Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn  
435 440 445

tgg gtg gaa aga aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg  
1392

Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu  
450 455 460

cac aat cac cac acg act aag agc ttc tcc cgg act ccg ggt aaa  
1437

His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys  
465 470 475

tgagaattc  
1446

<210> 12

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-IgG fusion

<220>

<221> misc\_feature

<222> (1)..(5)

<223> 3' end of secretory signal

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<221> misc\_feature

<222> (6)..(196)

<223> DRA\*0101 extracellular domain

<220>

<221> misc\_feature

<222> (197)..(203)

<223> Linker

<220>

<221> misc\_feature

<222> (204)..(243)

<223> Fos leucine zipper domain

<220>

<221> misc\_feature

<222> (244)..(479)

<223> IgG domain

<400> 12

Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu  
1 5 10 15

Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp  
20 25 30

Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp  
35 40 45

Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala  
50 55 60

Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys  
65 70 75 80

Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val  
85 90 95

Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys  
100 105 110

Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg  
115 120 125

Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro  
130 135 140

Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro  
145 150 155 160

Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp  
165 170 175

Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro  
180 185 190

Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Glu Thr Asp Thr Leu  
195 200 205

Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln Thr  
210 215 220

Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu  
225 230 235 240

Ala Ala His Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys  
245 250 255

Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val  
260 265 270

Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser

275					280					285					
Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp
290					295					300					
Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	Val	Glu	Val	His	Thr	Ala	Gln
305					310					315					320
Thr	Gln	Thr	His	Arg	Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg	Val	Val	Ser
				325					330					335	
Ala	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Met	Ser	Gly	Lys	Glu	Phe	Lys
			340					345					350		
Cys	Lys	Val	Asn	Asn	Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile
		355					360					365			
Ser	Lys	Pro	Lys	Gly	Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr	Val	Leu	Pro
	370					375					380				
Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys	Lys	Gln	Val	Thr	Leu	Thr	Cys	Met
385					390					395					400
Val	Thr	Asp	Phe	Met	Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn
				405					410					415	
Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys	Asn	Thr	Glu	Pro	Val	Leu	Asp	Ser
			420					425					430		
Asp	Gly	Ser	Tyr	Phe	Met	Tyr	Ser	Lys	Leu	Arg	Val	Glu	Lys	Lys	Asn
		435					440					445			
Trp	Val	Glu	Arg	Asn	Ser	Tyr	Ser	Cys	Ser	Val	Val	His	Glu	Gly	Leu
	450					455					460				
His	Asn	His	His	Thr	Thr	Lys	Ser	Phe	Ser	Arg	Thr	Pro	Gly	Lys	
465					470					475					

<210> 13

<211> 1851

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-IgM fusion

<220>

<221> CDS

<222> (1)..(1836)

<220>

<221> misc\_feature

<222> (1)..(75)

<223> 3' end of secretory signal

<220>

<221> misc\_feature

<222> (76)..(648)

<223> DRA\*0101 extracellular domain

<220>

<221> misc\_feature

<222> (649)..(669)

<223> Linker

<220>

<221> misc\_feature

<222> (670)..(789)

<223> Fos leucine zipper domain

<220>

<221> misc\_feature

<222> (790)..(1836)

<223> IgG domain

<400> 13

atg gcc ata agt gga gtc cct gtg cta gga ttt ttc atc ata gct gtg	48
Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val	
1 5 10 15	

ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc	96
Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile	
20 25 30	

atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg	
144	
Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met	
35 40 45	

ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag	
192	
Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys	
50 55 60	

gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag	
240	
Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu	
65 70 75 80	

gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa	
288	
Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu	
85 90 95	

atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca	
336	
Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro	
100 105 110	

gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac	
384	
Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn	
115 120 125	

gtc ctc atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc	
432	

Val	Leu	Ile	Cys	Phe	Ile	Asp	Lys	Phe	Thr	Pro	Pro	Val	Val	Asn	Val
130						135					140				
acg	tgg	ctt	cga	aat	gga	aaa	cct	gtc	acc	aca	gga	gtg	tca	gag	aca
480															
Thr	Trp	Leu	Arg	Asn	Gly	Lys	Pro	Val	Thr	Thr	Gly	Val	Ser	Glu	Thr
145					150					155					160
gtc	ttc	ctg	ccc	agg	gaa	gac	cac	ctt	ttc	cgc	aag	ttc	cac	tat	ctc
528															
Val	Phe	Leu	Pro	Arg	Glu	Asp	His	Leu	Phe	Arg	Lys	Phe	His	Tyr	Leu
				165					170					175	
ccc	ttc	ctg	ccc	tca	act	gag	gac	gtt	tac	gac	tgc	agg	gtg	gag	cac
576															
Pro	Phe	Leu	Pro	Ser	Thr	Glu	Asp	Val	Tyr	Asp	Cys	Arg	Val	Glu	His
			180					185					190		
tgg	ggc	ttg	gat	gag	cct	ctt	ctc	aag	cac	tgg	gag	ttt	gat	gct	cca
624															
Trp	Gly	Leu	Asp	Glu	Pro	Leu	Leu	Lys	His	Trp	Glu	Phe	Asp	Ala	Pro
		195					200					205			
agc	cct	ctc	cca	gag	act	aca	gag	gtc	gac	gga	ggt	ggc	ggc	ggt	tta
672															
Ser	Pro	Leu	Pro	Glu	Thr	Thr	Glu	Val	Asp	Gly	Gly	Gly	Gly	Gly	Leu
	210					215					220				
act	gat	aca	ctc	caa	gcg	gag	aca	gat	caa	ctt	gaa	gac	gag	aag	tct
720															
Thr	Asp	Thr	Leu	Gln	Ala	Glu	Thr	Asp	Gln	Leu	Glu	Asp	Glu	Lys	Ser
225					230					235					240
gcg	ttg	cag	acc	gag	att	gcc	aat	cta	ctg	aaa	gag	aag	gaa	aaa	ctg
768															
Ala	Leu	Gln	Thr	Glu	Ile	Ala	Asn	Leu	Leu	Lys	Glu	Lys	Glu	Lys	Leu
				245				250						255	
gag	ttc	atc	ctg	gcc	gcc	cac	gtc	gca	gaa	atg	aac	ccc	aat	gta	aat
816															
Glu	Phe	Ile	Leu	Ala	Ala	His	Val	Ala	Glu	Met	Asn	Pro	Asn	Val	Asn
			260					265					270		
gtg	ttc	gtc	cca	cca	cgg	gat	ggc	ttc	tct	ggc	cct	gca	cca	cgc	aag
864															
Val	Phe	Val	Pro	Pro	Arg	Asp	Gly	Phe	Ser	Gly	Pro	Ala	Pro	Arg	Lys
		275					280					285			
tct	aaa	ctc	atc	tgc	gag	gcc	acg	aac	ttc	act	cca	aaa	ccg	atc	aca
912															
Ser	Lys	Leu	Ile	Cys	Glu	Ala	Thr	Asn	Phe	Thr	Pro	Lys	Pro	Ile	Thr
	290					295					300				
gta	tcc	tgg	cta	aag	gat	ggg	aag	ctc	gtg	gaa	tct	ggc	ttc	acc	aca
960															
Val	Ser	Trp	Leu	Lys	Asp	Gly	Lys	Leu	Val	Glu	Ser	Gly	Phe	Thr	Thr
305					310					315					320



gat ccg gtg acc atc gag aac aaa gga tcc aca ccc caa acc tac aag  
1008  
Asp Pro Val Thr Ile Glu Asn Lys Gly Ser Thr Pro Gln Thr Tyr Lys  
325 330 335

gtc ata agc aca ctt acc atc tct gaa atc gac tgg ctg aac ctg aat  
1056  
Val Ile Ser Thr Leu Thr Ile Ser Glu Ile Asp Trp Leu Asn Leu Asn  
340 345 350

gtg tac acc tgc cgt gtg gat cac agg ggt ctc acc ttc ttg aag aac  
1104  
Val Tyr Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Leu Lys Asn  
355 360 365

gtg tcc tcc aca tgt gct gcc agt ccc tcc aca gat atc ctt aat ttt  
1152  
Val Ser Ser Thr Cys Ala Ala Ser Pro Ser Thr Asp Ile Leu Asn Phe  
370 375 380

act att cct cct tcc ttt gcc gac atc ttc ctt agc aag tcc gct aac  
1200  
Thr Ile Pro Pro Ser Phe Ala Asp Ile Phe Leu Ser Lys Ser Ala Asn  
385 390 395 400

ctg acc tgt ctg gtc tca aac ctg gca acc tat gaa acc ctg agt atc  
1248  
Leu Thr Cys Leu Val Ser Asn Leu Ala Thr Tyr Glu Thr Leu Ser Ile  
405 410 415

tcc tgg gct tct caa agt ggt gaa cca ctg gaa acc aaa att aaa atc  
1296  
Ser Trp Ala Ser Gln Ser Gly Glu Pro Leu Glu Thr Lys Ile Lys Ile  
420 425 430

atg gaa agc cat ccc aat ggc acc ttc agt gct aag ggt gtg gct agt  
1344  
Met Glu Ser His Pro Asn Gly Thr Phe Ser Ala Lys Gly Val Ala Ser  
435 440 445

gtt tgt gtg gaa gac tgg aat aac agg aag gaa ttt gtg tgt act gtg  
1392  
Val Cys Val Glu Asp Trp Asn Asn Arg Lys Glu Phe Val Cys Thr Val  
450 455 460

act cac agg gat ctg cct tca cca cag aag aaa ttc atc tca aaa ccc  
1440  
Thr His Arg Asp Leu Pro Ser Pro Gln Lys Lys Phe Ile Ser Lys Pro  
465 470 475 480

aat gag gtg cac aaa cat cca cct gct gtg tac ctg ctg cca cca gct  
1488  
Asn Glu Val His Lys His Pro Pro Ala Val Tyr Leu Leu Pro Pro Ala  
485 490 495

cgt gaa caa ctg aac ctg agg gag tca gcc aca gtc acc tgc ctg gtg  
1536  
Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Val Thr Cys Leu Val  
500 505 510

aag ggc ttc tct cct gca gac atc tct gtg caa tgg aag cag agg ggc  
1584

Lys Gly Phe Ser Pro Ala Asp Ile Ser Val Gln Trp Lys Gln Arg Gly

515 520 525  
cag ctc tta ccc cag gag aag tat gtg acc agt gcc ccg atg cca gag  
1632

Gln Leu Leu Pro Gln Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu  
530 535 540

cct ggg gcc cca ggc ttc tac ttt acc cac agc atc ctg act gtg aca  
1680

Pro Gly Ala Pro Gly Phe Tyr Phe Thr His Ser Ile Leu Thr Val Thr  
545 550 555 560

gag gag gaa tgg aac tcc gga gag acc tat acc tgt gtt gta ggc cac  
1728

Glu Glu Glu Trp Asn Ser Gly Glu Thr Tyr Thr Cys Val Val Gly His  
565 570 575

gag gcc ctg cca cac ctg gtg acc gag agg acc gtg gac aag tcc act  
1776

Glu Ala Leu Pro His Leu Val Thr Glu Arg Thr Val Asp Lys Ser Thr  
580 585 590

ggt aaa ccc aca ctg tac aat gtc tcc ctg atc atg tct gac aca ggc  
1824

Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly  
595 600 605

ggc acc tgc tat tgaagatctg tcgac  
1851

Gly Thr Cys Tyr  
610

<210> 14

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-IgM fusion

<220>

<221> misc\_feature

<222> (1)..(25)

<223> 3' end of secretory signal

<220>

<221> misc\_feature

<222> (26)..(216)

<223> DRA\*0101 extracellular domain

<220>

<221> misc\_feature

<222> (217)..(223)

<223> Linker

<220>  
 <221> misc\_feature  
 <222> (224)..(263)  
 <223> Fos leucine zipper domain

<220>  
 <221> misc\_feature  
 <222> (264)..(612)  
 <223> IgG domain

<400> 14

Met	Ala	Ile	Ser	Gly	Val	Pro	Val	Leu	Gly	Phe	Phe	Ile	Ile	Ala	Val
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Leu	Met	Ser	Ala	Gln	Glu	Ser	Trp	Ala	Ile	Lys	Glu	Glu	His	Val	Ile
			20					25					30		
Ile	Gln	Ala	Glu	Phe	Tyr	Leu	Asn	Pro	Asp	Gln	Ser	Gly	Glu	Phe	Met
		35					40					45			
Phe	Asp	Phe	Asp	Gly	Asp	Glu	Ile	Phe	His	Val	Asp	Met	Ala	Lys	Lys
	50						55				60				
Glu	Thr	Val	Trp	Arg	Leu	Glu	Glu	Phe	Gly	Arg	Phe	Ala	Ser	Phe	Glu
65					70					75					80
Ala	Gln	Gly	Ala	Leu	Ala	Asn	Ile	Ala	Val	Asp	Lys	Ala	Asn	Leu	Glu
				85					90					95	
Ile	Met	Thr	Lys	Arg	Ser	Asn	Tyr	Thr	Pro	Ile	Thr	Asn	Val	Pro	Pro
			100					105					110		
Glu	Val	Thr	Val	Leu	Thr	Asn	Ser	Pro	Val	Glu	Leu	Arg	Glu	Pro	Asn
		115					120					125			
Val	Leu	Ile	Cys	Phe	Ile	Asp	Lys	Phe	Thr	Pro	Pro	Val	Val	Asn	Val
	130					135					140				
Thr	Trp	Leu	Arg	Asn	Gly	Lys	Pro	Val	Thr	Thr	Gly	Val	Ser	Glu	Thr
145					150					155					160
Val	Phe	Leu	Pro	Arg	Glu	Asp	His	Leu	Phe	Arg	Lys	Phe	His	Tyr	Leu
				165					170					175	
Pro	Phe	Leu	Pro	Ser	Thr	Glu	Asp	Val	Tyr	Asp	Cys	Arg	Val	Glu	His
			180					185					190		
Trp	Gly	Leu	Asp	Glu	Pro	Leu	Leu	Lys	His	Trp	Glu	Phe	Asp	Ala	Pro
		195					200					205			
Ser	Pro	Leu	Pro	Glu	Thr	Thr	Glu	Val	Asp	Gly	Gly	Gly	Gly	Gly	Leu
	210					215					220				
Thr	Asp	Thr	Leu	Gln	Ala	Glu	Thr	Asp	Gln	Leu	Glu	Asp	Glu	Lys	Ser
225					230					235					240
Ala	Leu	Gln	Thr	Glu	Ile	Ala	Asn	Leu	Leu	Lys	Glu	Lys	Glu	Lys	Leu

245										250					255									
Glu	Phe	Ile	Leu	Ala	Ala	His	Val	Ala	Glu	Met	Asn	Pro	Asn	Val	Asn									
260										265					270									
Val	Phe	Val	Pro	Pro	Arg	Asp	Gly	Phe	Ser	Gly	Pro	Ala	Pro	Arg	Lys									
275										280					285									
Ser	Lys	Leu	Ile	Cys	Glu	Ala	Thr	Asn	Phe	Thr	Pro	Lys	Pro	Ile	Thr									
290										295					300									
Val	Ser	Trp	Leu	Lys	Asp	Gly	Lys	Leu	Val	Glu	Ser	Gly	Phe	Thr	Thr									
305										310					315					320				
Asp	Pro	Val	Thr	Ile	Glu	Asn	Lys	Gly	Ser	Thr	Pro	Gln	Thr	Tyr	Lys									
325										330					335									
Val	Ile	Ser	Thr	Leu	Thr	Ile	Ser	Glu	Ile	Asp	Trp	Leu	Asn	Leu	Asn									
340										345					350									
Val	Tyr	Thr	Cys	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Leu	Lys	Asn									
355										360					365									
Val	Ser	Ser	Thr	Cys	Ala	Ala	Ser	Pro	Ser	Thr	Asp	Ile	Leu	Asn	Phe									
370										375					380									
Thr	Ile	Pro	Pro	Ser	Phe	Ala	Asp	Ile	Phe	Leu	Ser	Lys	Ser	Ala	Asn									
385										390					395					400				
Leu	Thr	Cys	Leu	Val	Ser	Asn	Leu	Ala	Thr	Tyr	Glu	Thr	Leu	Ser	Ile									
405										410					415									
Ser	Trp	Ala	Ser	Gln	Ser	Gly	Glu	Pro	Leu	Glu	Thr	Lys	Ile	Lys	Ile									
420										425					430									
Met	Glu	Ser	His	Pro	Asn	Gly	Thr	Phe	Ser	Ala	Lys	Gly	Val	Ala	Ser									
435										440					445									
Val	Cys	Val	Glu	Asp	Trp	Asn	Asn	Arg	Lys	Glu	Phe	Val	Cys	Thr	Val									
450										455					460									
Thr	His	Arg	Asp	Leu	Pro	Ser	Pro	Gln	Lys	Lys	Phe	Ile	Ser	Lys	Pro									
465										470					475					480				
Asn	Glu	Val	His	Lys	His	Pro	Pro	Ala	Val	Tyr	Leu	Leu	Pro	Pro	Ala									
485										490					495									
Arg	Glu	Gln	Leu	Asn	Leu	Arg	Glu	Ser	Ala	Thr	Val	Thr	Cys	Leu	Val									
500										505					510									
Lys	Gly	Phe	Ser	Pro	Ala	Asp	Ile	Ser	Val	Gln	Trp	Lys	Gln	Arg	Gly									
515										520					525									
Gln	Leu	Leu	Pro	Gln	Glu	Lys	Tyr	Val	Thr	Ser	Ala	Pro	Met	Pro	Glu									
530										535					540									
Pro	Gly	Ala	Pro	Gly	Phe	Tyr	Phe	Thr	His	Ser	Ile	Leu	Thr	Val	Thr									
545										550					555					560				

Glu Glu Glu Trp Asn Ser Gly Glu Thr Tyr Thr Cys Val Val Gly His  
565 570 575

Glu Ala Leu Pro His Leu Val Thr Glu Arg Thr Val Asp Lys Ser Thr  
580 585 590

Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly  
595 600 605

Gly Thr Cys Tyr  
610